



JUN 07 2002

TECH CENTER 1600/2900

Raw Sequence Listing Error Summary .

SERIAL NUMBER: 09/689, 343B ERROR DETECTED SUGGESTED CORRECTION ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISII "ALPIIA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will Wrapped Aminos prevent "wrapping." Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces. The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; Misaligned Amino Numbering use space characters, instead. The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please Non-ASCII ensure your subsequent submission is saved in ASCII text. contain n's or Xaa's representing more than one residue. Per Sequence Rules, Variable Length each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<23> section that some may be missing. PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid "bug" Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. Skipped Sequences Sequence(s)_ missing. If intentional, please insert the following lines for each skipped sequence. (NEW RULES) <210> sequence id number <400> sequence id number 000 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing. (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence Use of <220> Sequence(s)_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See 'Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 06/04/2001



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/689, 3433
Source: 1636
Date Processed by STIC: 5-30-02

-- JUN 0 7 2002

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
- 3. Hand Carry directly to:
 U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
 - U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
- 4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002





JUN 07 2002

1636

TECH CENTER 1600/2900

RAW SEQUENCE LISTING DATE: 05/30/2002 PATENT APPLICATION: US/09/689,343B TIME: 10:22:31

Input Set : A:\NEB-181.ST25.txt

```
2 <110> APPLICANT: Vaisvila, Romualdus
             Morgan, Richard D.
      3
             Kucera, Rebecca B.
      4
             Claus, Toby B.
             Raleigh, Elisabeth A.
      8 <120> TITLE OF INVENTION: Method For Cloning And Producing The MseI Restriction
Endonuclease
    10 <130> FILE REFERENCE: NEB-181
     12 <140> CURRENT APPLICATION NUMBER: US 09/689,343B
     13 <141> CURRENT FILING DATE: 2000-10-12
     15 <160> NUMBER OF SEQ ID NOS: 9
    17 <170> SOFTWARE: PatentIn version 3.1
     19 <210> SEO ID NO: 1
     20 <211> LENGTH: 903
     21 <212> TYPE: DNA
     22 <213> ORGANISM: Micrococcus sp.
     24 <220> FEATURE:
    25 <221> NAME/KEY: CDS
    26 <222> LOCATION: (1)..(900)
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    34 gag gcg gac aac etc gat ttc att caa acg etc ecc gac gcg age ttc
                                                                               96
    35 Glu Ala Asp Asn Leu Asp Phe Ile Gln Thr Leu Pro Asp Ala Ser Phe
                   20
                                        25
    38 cga atg atc tac atc gat ccg ccg ttc aac aca ggg cga acg cag cgg
    39 Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
                                    40
    42 ctt cag tcg ctc aag acg acc cgc tcg gtc aca ggg tcg cga gtc ggc
                                                                              192
    43 Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
                                55
    46 ttc aaa ggc cag acg tac gac acg gtc aag agc act ctg cac tcg tat
                                                                              240
    47 Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
    48 65
                            70
    50 gac gac gct ttc acc gac tat tgg tcg ttc ctc gaa ccg cgt ctc ctg
                                                                              288
    51 Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
    54 gag get tgg egg ttg etc ace eet gae gge geg etc tat ett eat etg
                                                                              336
    55 Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu
                   100
    58 gat tac ege gag gtt cae tae gee aag gte gte ete gae geg atg tte
                                                                              384
    59 Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe
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RAW SEQUENCE LISTING DATE: 05/30/2002 PATENT APPLICATION: US/09/689,343B TIME: 10:22:31

Input Set : A:\NEB-181.ST25.txt

| 60 115 120 125 | |
|---|------|
| 62 gga cgc gaa agc ttc ctg aac gag ctg atc tgg gcg tac gac tac ggc | 432 |
| 63 Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly | |
| 64 130 135 140 | |
| 66 gcg cgc tcg aag agc aag tgg ccc acc aag cac gac aac atc ctc gtg | 480 |
| 67 Ala Arg Ser Lys Ser Lys Trp Pro Thr Lys His Asp Asn Ile Leu Val | |
| 68 145 150 155 160 | |
| 70 tat gtg aag gac ccg aac aac tac gtc tgg aac ggt cag gat gta gat | 528 |
| 71 Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp | |
| 72 165 170 175 | |
| 74 cgc gag ccc tac atg gcg ccc ggg ctc gtt aca ccc gag aag gta gcg | 576 |
| 75 Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala | |
| 76 180 185 190 | |
| 78 ctt ggc aag ctg ccc acc gac gtc tgg tgg cac aca atc gtt ccg cct | 624 |
| 79 Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro | |
| 80 195 200 205 | |
| 82 gcg agc aaa gag cgc acc ggg tac gcg aca cag aag ccg gtc ggc atc | 672 |
| 83 Ala Ser Lys Glu Arg. Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile | |
| 84 210 215 220 | |
| 86 atc cgt cgc atg att cag gcg agc agc aat gaa ggc gac tgg gtt ctg | 720 |
| 87 Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu | |
| 88 225 230 235 240 | |
| 90 gat ttc ttc gct ggt agt ggg acg acc ggc gcc gcc cgc cag ctc | 768 |
| 91 Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu | |
| 92 245 250 255 | |
| 94 gga cgc cgt ttt gtg ctc gta gac gtc aac cca gaa gca atc gcg gta | 816 |
| 95 Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val | |
| 96 260 265 270 | |
| 98 atg gca aaa cgg ttg gat gac ggg gca ttg gac acc agc gtg acg atc | 864 |
| 99 Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile | |
| 100 275 280 285 | 0.00 |
| 102 gtg cag act ccc cag agt gac cca cga acc gac gga tga | 903 |
| 103 Val Gln Thr Pro Gln Ser Asp Pro Arg Thr Asp Gly | |
| 104 290 295 300 | |
| 107 <210> SEQ ID NO: 2 | |
| 108 <211> LENGTH: 300 | |
| 109 <212> TYPE: PRT | |
| 110 <213> ORGANISM: Micrococcus sp. | |
| 112 <400> SEQUENCE: 2 114 Met Pro Ile Ser Thr Val Trp Thr Pro Asp Gly Asp Asp Leu Ile Val | |
| 114 Met 210 11e sel 111 val 11p 111 210 Asp Gly Asp Asp Leu 11e val 115 1 5 10 15 | |
| 118 Glu Ala Asp Asn Leu Asp Phe Ile Gln Thr Leu Pro Asp Ala Ser Phe | |
| 110 GIU AIA ASP ASII LEU ASP PHE 11E GIII THI LEU PIO ASP AIA SEI PHE 119 20 25 30 | |
| 122 Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg | |
| 122 And Met The Tyl The Asp Flo | |
| 126 Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly | |
| 127 50 55 60 | |
| 130 Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr | |
| 131 65 70 75 80 | |
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/689,343B

DATE: 05/30/2002 TIME: 10:22:32

Input Set : A:\NEB-181.ST25.txt

| | | | | • | 21 | | • | | • | | • | | | | | | | | |
|------------|------|-------|-------|--------------|---|--------|-------|-------|-------|-----------|-----|------------|------------|----------------------|-----------|---------|---------|-----------------|------|
| 134 135 | Asp | Asp | Ala | Phe | Thr 85 | Asp | Tyr | Trp | Ser | Phe 90 | Leu | Glu | Pro | Arg | Leu 95 | Leu | | | |
| | Glu | Δla | Trn | Arg | | T.e.11 | Thr | Pro | Asn | - | Δla | Leu | Tvr | Leu | - | Leu | | | |
| 139 | Olu | u | 115 | 100 | Lcu | | | 110 | 105 | | | | -1- | 110 | | | | | |
| | Asp | Tyr | Arq | Glu | Val | His | Tyr | Ala | | | Val | Leu | Asp | | Met | Phe | | | |
| 143 | - | • | 115 | | | | - | 120 | - | | | | 125 | | | | | | |
| 146 | Gly | Arg | Glu | Ser | Phe | Leu | Asn | Glu | Leu | Ile | Trp | Ala | Tyr | Asp | Tyr | Gly | | | |
| 147 | | 130 | | | | | 135 | | | | | 140 | | | | | | | |
| | | Arg | Ser | Lys | Ser | - | Trp | Pro | Thr | Lys | | Asp | Asn | Ile | Leu | | | | |
| | 145 | | _ | _ | _ | 150 | _ | _ | 1 | _ | 155 | a 1 | a 1 | | | 160 | | | |
| | Tyr | vaı | Lys | Asp | | Asn | Asn | Tyr | vaı | | Asn | GIY | GIN | ASP | 175 | Asp | | | |
| 155 | λνα | Clu | Dro | Tyr | 165 Mot | λla | Dro | C1 v | Lou | 170 | Thr | Dro | Glu | T.vc | | λla | | | , |
| 159 | мту | Giu | PIU | 180 | Met | Ата | FIU | GLY | 185 | | | · | | 190 | Vul | AIU | | | |
| | Leu | Glv | Lvs | Leu | Pro | Thr | Asp | val | | | | | | | Pro | Pro | | | |
| 163 | 204 | 011 | 195 | | | | | 200 | | | | | 205 | | | | | | |
| | Ala | Ser | | Glu | Arg | Thr | Gly | Tyr | | | | | Pro | Val | Gly | Ile | | | |
| 167 | | 210 | _ | | _ | | 215 | - | | | | 220 | | | | | | | |
| 170 | Ile | Arg | Arg | Met | Ile | Gln | Ala | Ser | Ser | Asn | Glu | Gly | Asp | ${\tt Trp}$ | Val | Leu | | | |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 | | | |
| | Asp | Phe | Phe | Ala | | Ser | Gly | Thr | Thr | | Ala | Ala | Ala | Arg | | Leu | | | |
| 175 | | _ | _ | | 245 | _ | | _ | | 250 | _ | a 1 | | | 255 | 1 | | | |
| | GLY | Arg | Arg | Phe | Val | Leu | Val | Asp | | Asn | Pro | GLu | Ala | | Ата | vaı | | | |
| 179 | Mot | 7 l a | Twe | 260 Arg | LOU | λan | λen | Clv | 265 | Lau | λen | Thr | Sar | 270 Val | Thr | Tlo | | | |
| 183 | Mec | Ата | 275 | ALG | цец | кър | дор | 280 | АІС | пец | АЗР | 1111 | 285 | vai | 1111 | 116 | | | |
| | Val | Gln | | Pro | Gln | Ser | Asp | | Arq | Thr | Asp | Gly | 200 | | | | | | |
| 187 | | 290 | | | | | 295 | | , | | _ | 300 | | | | | | | |
| 190 | <210 | 0> S! | EQ II | ON C | : 3 | | | | | | | | | | | | | | |
| | | | | H: 12 | | | | | _ | | | 50 | _ | . 1 . | | | | | |
| | | | | DNA | | | | | 7. | | | J € | | 140 | n q | | 10 | m | |
| | | | | ISM: | Envi | Lron | nenta | al Di | NA | | | 5. | | c. | | | | m successive | 1 |
| | | | EATU | | CDC | | | | | | . < | 11 | 0/ | טע | برممر | MAG | کنخ | SHE | _e + |
| | | | - | KEY: ION: | | /11 | 3331 | | | | | | | | | | ノ | | |
| | | | | INFO | | | | | | | | Th | n hma | n6 a | U | | | | |
| | | | EATUI | | ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, | | • | | | | | វ៉ាe | Seque | יו שווטו יו שווטו | S SNOW | m exist | through | out | |
| | | | | KEY: | misc | _fea | ature | 3 | | | | | uence | | | | heck su | out bsequent | |
| | | | | ION: | | | | | | | | • | | 0. 011 | unai Ci | 1015. | | | |
| | | | | INF | | | | | any a | amino | aci | ld | | | | | | | |
| | | | EATUI | | | | | | | | | | | | | | | | |
| | | | | KEY: | | | | | | | | | | | | | | | |
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| | | | | INFO | | TON: | N= | G, A | A, C | or ' | : | | | | | | | | |
| | | | | NCE: | | taa | aaa | aa+ | 222 | Car | ++= | agg | tto | CCP | CCP | act | | 48 | |
| | | | | Leu | | | | | | | | | | | | | | 40 | |
| 213 | | 110 | T 11T | Leu | 5 | 115 | 110 | OTY | כיות | 10 | ⊥÷u | ٦٥٦ | ı ne | 110 | 15 | 23.IU | | | |
| | | tcc | ttq | cat | - | qaq | aqt | qta | qtc | | qaq | qqa | qcq | gag | | ccq | | 96 | |
| | | | | | - , | | / | 5 - 5 | J | | ر د | J J | J . J | | | | | | |





RAW SEQUENCE LISTING DATE: 05/30/2002 PATENT APPLICATION: US/09/689,343B TIME: 10:22:32

Input Set : A:\NEB-181.ST25.txt

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| | 219 | cct | aat | cat | cta | att | t.aa | aca | gac | aac | ct.a | cca | cta | atα | αta | αat | ttα | | 144 |
| | | | | | | Ile | | | | | | | | | | | | | |
| | | PIO | ASII | | neu | TIE | пъ | Ата | _ | ASII | neu | PIO | Leu | | vaı | ASP | nea | | |
| | 221 | | | 35 | | | | | 40 | | | | | 45 | | | | | |
| | 223 | ttg | gcc | gaa | tat | gaa | ggg | aaa | atc | gat | ctg | atc | tac | gcc | gat | CCC | cct | | 192 |
| | 224 | Leu | Ala | Glu | Tyr | Glu | Gly | Lys | Ile | Asp | Leu | Ile | Tyr | Ala | Asp | Pro | Pro | | |
| | 225 | | 50 | | - | | - | 55 | | - | | | 60 | | ~ | | | | |
| | | +++ | | асп | nat | cgt | act | | aca | aca | спа | att | aat | cat | aaa | a a a | ant | | 240 |
| | | | | | | | | | | | | | | | | | | | 240 |
| | | | Pne | THE | ASP | Arg | | TAL | Ald | Ата | Arg | | GIY | HIS | GIY | GIU | _ | | |
| | 229 | | | | | | 70 | | | | | 75 | | | | | 80 | | |
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| | 232 | Ser | Arq | Arq | Pro | Gln | Thr | Trp | Gln | Leu | Ala | Glu | Gly | Tyr | Thr | Asp | Glu | | |
| | 233 | | _ | _ | | 85 | • | - | | | 90 | | - | - | | 95 | | | |
| | | + aa | 220 | aat | ++= | gat | ~ a a | t = 0 | α±ά | nan | | att | + = + | 002 | 000 | | at a | | 336 |
| | | | | | | | | | | | | | | | | | | | 330 |
| | | Trp | гàг | Asp | | Asp | GIU | Tyr | ьeu | _ | Pne | Leu | Tyr | Pro | _ | Leu | val | | |
| | 237 | | | | 100 | | | | | 105 | | | | | 110 | | | | |
| | 239 | ctg | atg | tat | cga | ctg | ctg | gca | cca | cac | gga | acg | ctc | tac | ttg | cac | ctg | | 384 |
| | 240 | Leu | Met | Tyr | Arq | Leu | Leu | Ala | Pro | His | Gly | Thr | Leu | Tyr | Leu | His | Leu | | |
| | 241 | | | 115 | , | | | | 120 | | - | | | 125 | | | | | |
| | | a 2 a | + ~~ | | aaa | aat | aaa | + 2.0 | | aat | at a | a+ a | a++ | | ~~~ | 2+0 | ++0 | | 432 |
| | | | | | | | | | | | | | | | | | | | 432 |
| | | Asp | | Hls | Ата | Asn | Ala | | vaı | Arg | vaı | ьeu | | Asp | GLu | тте | Pne | | |
| | 245 | | 130 | | | | | 135 | | | | | 140 | | | | | | |
| | 247 | ggg | cga | cag | cgg | ttt | ctc | aac | gag | atc | gtc | tgg | atc | tat | cac | ggc | CCC | | 480 |
| | | | | | | Phe | | | | | | | | | | | | | |
| | 249 | _ | , | | | | 150 | | | | | 155 | | - | _ | - 4 | 160 | | |
| | | | 000 | ato | 002 | cgc | | ++0 | 220 | 000 | 222 | | ant. | 3.00 | 2+0 | ++~ | | | 528 |
| | | | | | | | | | | | | | | | | | | | 320 |
| | | ser | Ата | ire | Arg | Arg | Ата | Pne | Lys | Arg | | HlS | Asp | Thr | тте | | Val | | |
| | 253 | | | | | 165 | | | | | 170 | | • | | | 175 | | | |
| | 255 | tat | gtg | aaa | ggt | gaa | aac | tat | aca | .ttc | aat | gcg | gat | gcg | gtt | cgt | caa | | 576 |
| | 256 | Tvr | Val | Lvs | Gly | Glu | Asn | Tvr | Thr | Phe | Asn | Ala | Asp | Ala | Val | Ara | Gln | | |
| | 257 | 4 | | | 180 | | | | | 185 | | | | | 190 | , | | | |
| | | cat | +20 | ast | | agc | 300 | ast | | | ++~ | aa+ | + a a | +00 | | 224 | ~~ | | 624 |
| | | | | | | | | | | | | | | | | | | | 024 |
| > | | Pro | Tyr | | Pro | Ser | xaa | HIS | | Thr | Pne | АТа | ser | | Pro | Lys | Ата | | |
| | 261 | | | 195 | | | | | 200 | | | | | 205 | | | | | |
| | 263 | ggc | ttt | ggt | aag | gtg | ccg | gat | ctg | cag | cgc | ggc | aaa | gtg | CCC | gaa | gac | | 672 |
| | 264 | Gly | Phe | Gly | Lys | Val | Pro | Asp | Leu | Gln | Arg | Gly | Lys | Val | Pro | Glu | Asp | | |
| | 265 | | 210 | _ | _ | | | 215 | | | _ | _ | 220 | | | | _ | | |
| | | taa | | tat | +++ | ccg | atc | | acc | cat | cta | cac | | gaa | caa | 200 | ααα | | 720 |
| | | | | | | | | | | | | | | | | | | | 720 |
| | | | пр | тАт | Pne | Pro | | Val | Ата | Arg | Leu | | AIG | GIU | Arg | ser | _ | | |
| | 269 | | | | | | 230 | | | | | 235 | | | | | 240 | | |
| | | | | | | aag | | | | | | | | | | | | | 768 |
| | 272 | Tyr | Pro | Thr | Gln | Lys | Pro | Gln | Ala | Leu | Leu | Glu | Arg | Ile | Leu | Leu | Ala | | |
| | 273 | _ | | | | 245 | | | | | 250 | | - | | | 255 | | | |
| | | tcc | tea | aac | aca | ggc | gat | cta | ata | aca | | tta | tto | tac | aac | | aaa | | 816 |
| | | | | | | | | | | | | | | | | | | | 010 |
| | | 261 | 261 | ASII | | Gly | ASP | ьeu | val | | ASP | rne | rne | Cys | _ | ser | ату | | |
| | 277 | | | | 260 | | | | | 265 | | | | | 270 | | | | |
| | | | | | | gtg | | | | | | | | | | | | • | 864 |
| | 280 | Thr | Thr | Ala | Val | Val | Ala | Ala | Arg | Leu | Gly | Arg | Arg | Phe | Leu | Val | Asn | | |
| | | | | | | | | | | | | | | | | | | | |





RAW SEQUENCE LISTING DATE: 05/30/2002 PATENT APPLICATION: US/09/689,343B TIME: 10:22:32

Input Set : A:\NEB-181.ST25.txt

| | | | | | | | | | | | | | 205 | | | | |
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| 281 | | | 275 | | * | | | 280 | | | | | 285 | | | | 0.1.0 |
| | | gca | | | | | | | | | | | | | | | 912 |
| | - | Ala | Ser | Trp | Arg | Ala | | His | Val | Thr | Arg | | Arg | Leu | Leu | Arg | |
| 285 | | 290 | | | | | 295 | | | | | 300 | | | | | |
| | | gga | | | | | | | | | | | | | | | 960 |
| | | Gly | Val | Ser | Phe | | Phe | Glu | Arg | Gln | | Thr | Phe | Thr | Leu | | |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| | | cag | | | | | _ | | _ | | | _ | | | - | | 1008 |
| | Ile | Gln | Pro | Leu | | Pro | Asp | \mathtt{Trp} | Leu | | Ile | Ala | Glu | Glu | | Ile | |
| 293 | | | | | 325 | | | | | 330 | | | | | 335 | | |
| | _ | ctc | | - | | | | _ | - | | - | - | | | - | | 1056 |
| | Arg | Leu | Gln | | Pro | Phe | Leu | Val | _ | Phe | \mathtt{Trp} | Glu | Val | _ | Asp | Gln | |
| 297 | | | | 340 | | | | | 345 | | | | | 350 | | | |
| | | - | | | | | _ | _ | _ | | | | | - | | _ | . 1104 |
| 300 | Trp | Asp | _ | Lys | Ile | Phe | Arg | | Arg | His | Gln | Gly | | Arg | Ser | Arg | |
| 301 | | | 355 | | | | | 360 | | | | | 365 | | | | |
| 303 | ctt | cag | gag | cag | gcg | ccg | ctc | tct | cta | cca | ttg | acc | ggg | aat | gga | ctg | 1152 |
| 304 | Leu | Gln | Glu | Gln | Ala | Pro | Leu | Ser | Leu | Pro | Leu | Thr | Gly | Asn | Gly | Leu | |
| 305 | | 370 | | | | | 375 | | | | | 380 | | | | | |
| | _ | tgt | - | | - | | - | _ | - | | _ | | | | | | 1200 |
| 308 | Leu | Cys | Val | Arg | Val | Val | Ser | Arg | Glu | Gly | Glu | Tyr | Tyr | Glu | Phe | Thr | |
| 309 | 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| | | cga | _ | - | - | | | | _ | - | | tga | | | | | 1236 |
| 312 | Gly | Arg | Ala | Asp | Ser | Pro | His | Pro | Val | Ser | Phe | | | | | | |
| | | | | | | | | | | | | | | | | | |
| 313 | | | | | 405 | | | | | 410 | | | | | | | |
| | <21 | 0> S1 | EQ II | ONO: | | | | | | 410 | | | | | | | |
| 316 317 | <21 | 1> LI | ENGT | H: 41 | : 4 | | | | | | | | | | | • | |
| 316 317 318 | <21: | 1> L1 2> T | ENGTI YPE: | H: 41 PRT | 11 | | | | | | C | 2.6 | 00 | i (1 | . 3 | • | |
| 316 317 318 319 | <21: <21: <21: | 1> L1 2> T 3> O | ENGTI YPE: RGANI | H: 41 PRT ISM: | 11 | ironn | | al Di | NA | | - J. | ll | ρο | i ze | . 3 | • | |
| 316 317 318 319 321 | <21: <21: <21: <22: | 1> L1 2> T3 3> O1 0> F1 | ENGTI YPE: RGANI EATUI | H: 41 PRT ISM: RE: | Envi | | | | NA . | | - S. | ll | Po | i ge | . 3 | , | |
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| 316 317 318 319 321 322 323 | <21: <21: <21: <22: <22: <22: | 1> L1 2> T1 3> O1 0> F1 1> NA 2> L0 | ENGTI YPE: RGANI EATUI AME/I DCATI | PRT ISM: RE: KEY: ION: | Envi | fea | ture (198) | e) | | | | | Po | i Se | . 3 | • | |
| 316 317 318 319 321 322 323 324 | <21: <21: <22: <22: <22: <22: <22: | 1> Li 2> TY 3> OF 0> FI 1> NA 2> LO 3> OF | ENGTH YPE: RGANI EATUH AME/H OCATI THER | H: 41 PRT ISM: RE: KEY: ION: | Envi | fea | ture (198) | e) | | | | | Po | i Gr | . 3 | , | |
| 316 317 318 319 321 322 323 324 328 | <21: <21: <22: <22: <22: <22: <40: | 1> Li 2> TY 3> Oi 0> Fi 1> Ni 2> Lo 3> Of 0> Si | ENGTH YPE: RGANI EATUH AME/H DCATI FHER EQUEN | H: 41 PRT ISM: RE: KEY: ION: INFO | Envi | c_fea 3)(TION: | ature (198) | e) 1 = 8 | any a | amino | o aci | id. | | | | | |
| 316 317 318 319 321 322 323 324 328 330 | <21: <21: <22: <22: <22: <22: <40: Met | 1> Li 2> TY 3> OF 0> FI 1> NA 2> LO 3> OF | ENGTH YPE: RGANI EATUH AME/H DCATI FHER EQUEN | H: 41 PRT ISM: RE: KEY: ION: INFO | Envi | c_fea 3)(TION: | ature (198) | e) 1 = 8 | any a | amino | o aci | id. | | | | | |
| 316 317 318 319 321 322 323 324 328 330 331 | <21: <21: <22: <22: <22: <22: <40: Met | 1> LI 2> TY 3> OI 0> FI 1> NA 2> LO 3> OY 0> SI Pro | ENGTH YPE: RGANI EATUH AME/H DCATI HER EQUEN | H: 41 PRT ISM: RE: KEY: ION: INFO NCE: Leu | miso (198 ORMAT 4 Asp | c_fea 3)(TION: | ture (198) Xaa | e a = a Gly | nny a | amino Gln | aci | id Ser | Phe | Pro | Pro 15 | Ala | |
| 316 317 318 319 321 322 323 324 328 330 331 334 | <21: <21: <22: <22: <22: <22: <40: Met | 1> Li 2> TY 3> Oi 0> Fi 1> Ni 2> Lo 3> Of 0> Si | ENGTH YPE: RGANI EATUH AME/H DCATI HER EQUEN | H: 41 PRT ISM: RE: RE: ION: INFO NCE: Leu His | miso (198 ORMAT 4 Asp | c_fea 3)(TION: | ture (198) Xaa | e a = a Gly | nny a Lys Val | amino Gln | aci | id Ser | Phe | Pro Glu | Pro 15 | Ala | |
| 316 317 318 319 321 322 323 324 328 330 331 334 335 | <21: <21: <22: <22: <22: <22: <400 Met 1 Thr | 1> Li 2> TY 3> OI 0> FI 1> NA 2> LO 3> OY 0> SI Pro | ENGTH YPE: RGANI EATUH AME/H DCATI HER EQUEN Thr | H: 41 PRT ISM: RE: CEY: ION: INFO NCE: Leu His 20 | miso (198 Asp 5 Leu | c_fea 3)(FION: Trp | Tature (198) Xaa Pro | Gly Val | uny a Lys Val 25 | Gln 10 Thr | Leu Glu | id Ser Gly | Phe Ala | Pro Glu 30 | Pro 15 Ser | Ala Pro | |
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| 316 317 318 319 321 322 323 324 328 330 331 334 335 338 339 | <21: <21: <22: <22: <22: <22: <40: Met 1 Thr | 1> LI 2> TY 3> OI 0> FI 1> NA 2> LO 3> OY 0> SI Pro Ser Asn | ENGTH YPE: RGANI RGATUH AME/H DCATI HER EQUEN Thr Leu Arg 35 | PRT PRT ISM: CEY: ON: INFO NCE: Leu His 20 Leu | Envi | c_fea 3)(TION: Trp Glu | Pro Ser | Gly Val Asp | Lys Val 25 Asn | Gln 10 Thr | Leu Glu Pro | id Ser Gly Leu | Phe Ala Met 45 | Pro Glu 30 Val | Pro 15 Ser Asp | Ala Pro Leu | |
| 316 317 318 319 321 322 323 324 328 330 331 334 335 338 339 342 | <21: <21: <22: <22: <22: <22: <40: Met 1 Thr | 1> L1 2> T3 3> O1 0> F1 1> NA 2> L0 3> O3 0> S1 Pro Ser Asn | ENGTH YPE: RGANI RGATUH AME/H DCATI HER EQUEN Thr Leu Arg 35 | PRT PRT ISM: CEY: ON: INFO NCE: Leu His 20 Leu | Envi | c_fea 3)(TION: Trp Glu | Pro Ser Ala | Gly Val Asp | Lys Val 25 Asn | Gln 10 Thr | Leu Glu Pro | id Ser Gly Leu | Phe Ala Met 45 | Pro Glu 30 Val | Pro 15 Ser Asp | Ala Pro Leu | |
| 316 317 318 319 321 322 323 324 328 330 331 334 335 338 339 342 343 | <21: <21: <22: <22: <22: <40: Met 1 Thr Pro | 1> L1 2> TY 3> OI 0> FI 1> NA 2> L0 3> OY 0> SI Pro Ser Asn Ala 50 | ENGTH YPE: RGANI RGATUH AME/H DCATI HER EQUEN Thr Leu Arg 35 Glu | PRT PRT ISM: CEY: ON: INFO NCE: Leu His 20 Leu Tyr | Envi misc (198 ORMAT 4 Asp 5 Leu Ile | c_fea 3)(TION: Trp Glu Trp | Pro Ser Ala Lys | Gly Val Asp 40 Ile | Lys Val 25 Asn | Gln 10 Thr Leu | Leu Glu Pro Ile | id Ser Gly Leu Tyr 60 | Phe Ala Met 45 Ala | Pro Glu 30 Val Asp | Pro 15 Ser Asp Pro | Ala Pro Leu Pro | |
| 316 317 318 319 321 322 323 324 328 330 331 335 338 339 342 343 346 | <21: <21: <22: <22: <22: <22: <400 Met 1 Thr Pro Leu Phe | 1> L1 2> T3 3> O1 0> F1 1> NA 2> L0 3> O3 0> S1 Pro Ser Asn | ENGTH YPE: RGANI RGATUH AME/H DCATI HER EQUEN Thr Leu Arg 35 Glu | PRT PRT ISM: CEY: ON: INFO NCE: Leu His 20 Leu Tyr | Envi misc (198 ORMAT 4 Asp 5 Leu Ile | c_fea 3)(FION: Trp Glu Trp Gly Thr | Pro Ser Ala Lys | Gly Val Asp 40 Ile | Lys Val 25 Asn | Gln 10 Thr Leu | Leu Glu Pro Ile | id Ser Gly Leu Tyr 60 | Phe Ala Met 45 Ala | Pro Glu 30 Val Asp | Pro 15 Ser Asp Pro | Ala Pro Leu Pro Asp | |
| 316 317 318 319 321 322 323 324 328 330 331 334 335 342 343 346 347 | <21: <21: <22: <22: <22: <400 Met 1 Thr Pro Leu Phe 65 | 1> L1 2> TY 3> OI 0> FI 1> NA 2> L0 3> OY 0> SI Pro Ser Asn Ala 50 Phe | ENGTH YPE: RGANT RGATUH AME/H DCATT HER EQUEN Thr Leu Arg 35 Glu | PRT PRT ISM: CEY: CON: INFO NCE: Leu His 20 Leu Tyr Asp | miso (198 ORMAT 4 Asp 5 Leu Ile Glu Arg | C_fea 3)(FION: Trp Glu Trp Gly Thr | Pro Ser Ala Lys 55 | Gly Val Asp 40 Ile | Lys Val 25 Asn Asp | Gln 10 Thr Leu Leu | Leu Glu Pro Ile Ile 75 | ser Gly Leu Tyr 60 Gly | Phe Ala Met 45 Ala | Pro Glu 30 Val Asp | Pro 15 Ser Asp Pro Glu | Ala Pro Leu Pro Asp 80 | |
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| 316 317 318 319 321 322 323 324 328 330 331 334 335 342 343 346 347 350 351 | <21: <21: <22: <22: <22: <22: <400 Met 1 Thr Pro Leu Phe 65 Ser | 1> L1 2> TY 3> OF 0> FI 1> NA 2> L0 3> OF 0> SI Pro Ser Asn Ala 50 Phe Arg | ENGTH YPE: RGANT RGATUH AME/H DCATT HER EQUEN Thr Leu Arg 35 Glu Thr | PRT PRT ISM: CEY: CON: INFO NCE: Leu His 20 Leu Tyr Asp Pro | miso (1980) CRMATA 4 Asp 5 Leu Ile Glu Arg Gln 85 | C_fea 3)(FION: Trp Glu Trp Gly Thr 70 | Pro Ser Ala Lys 55 Tyr | Gly Val Asp 40 Ile Ala Gln | Lys Val 25 Asn Asp Ala | Gln 10 Thr Leu Leu Arg | Leu Glu Pro Ile Ile 75 Glu | ser Gly Leu Tyr 60 Gly | Phe Ala Met 45 Ala His | Pro Glu 30 Val Asp Gly | Pro 15 Ser Asp Pro Glu Asp 95 | Ala Pro Leu Pro Asp 80 Glu | |
| 316 317 318 319 321 322 323 324 328 330 331 334 335 342 343 347 350 351 354 | <21: <21: <22: <22: <22: <22: <400 Met 1 Thr Pro Leu Phe 65 Ser | 1> L1 2> TY 3> OI 0> FI 1> NA 2> L0 3> OY 0> SI Pro Ser Asn Ala 50 Phe | ENGTH YPE: RGANT RGATUH AME/H DCATT HER EQUEN Thr Leu Arg 35 Glu Thr | PRT PRT ISM: CEY: CON: INFO NCE: Leu His 20 Leu Tyr Asp Pro Leu | miso (1980) CRMATA 4 Asp 5 Leu Ile Glu Arg Gln 85 | C_fea 3)(FION: Trp Glu Trp Gly Thr 70 | Pro Ser Ala Lys 55 Tyr | Gly Val Asp 40 Ile Ala Gln | Lys Val 25 Asn Asp Ala Leu Asp | Gln 10 Thr Leu Leu Arg | Leu Glu Pro Ile Ile 75 Glu | ser Gly Leu Tyr 60 Gly | Phe Ala Met 45 Ala His | Pro Glu 30 Val Asp Gly Thr | Pro 15 Ser Asp Pro Glu Asp 95 | Ala Pro Leu Pro Asp 80 Glu | |
| 316 317 318 319 321 322 323 324 330 331 334 335 342 343 346 347 350 351 354 355 | <21: <21: <22: <22: <22: <400 Met 1 Thr Pro Leu Phe 65 Ser Trp | 1> L1 2> TY 3> OF 0> FI 1> NA 2> L0 3> OF 0> SI Pro Ser Asn Ala 50 Phe Arg | ENGTH YPE: RGANT REATUR AME/R CCATT FHER EQUEN Thr Leu Arg 35 Glu Thr Arg | PRT PRT ISM: CEY: CON: INFO NCE: Leu His 20 Leu Tyr Asp Pro Leu 100 | miso (198 ORMAT 4 Asp 5 Leu Ile Glu Arg Gln 85 Asp | C_fea 3)(FION: Trp Glu Trp Gly Thr 70 Thr | Pro Ser Ala Lys 55 Tyr Trp | Gly Val Asp 40 Ile Ala Gln Leu | Lys Val 25 Asn Asp Ala Leu Asp | amino Gln 10 Thr Leu Arg Ala 90 Phe | Leu Glu Pro Ile 75 Glu Leu | Ser Gly Leu Tyr 60 Gly Gly | Phe Ala Met 45 Ala His Tyr | Pro Glu 30 Val Asp Gly Thr Arg | Pro 15 Ser Asp Pro Glu Asp 95 Leu | Ala Pro Leu Pro Asp 80 Glu Val | |





RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/689,343B

DATE: 05/30/2002 TIME: 10:22:33

Input Set : A:\NEB-181.ST25.txt

Output Set: N:\CRF3\05302002\1689343B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the $\langle 220 \rangle$ to $\langle 223 \rangle$ fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 594
Seq#:3; Xaa Pos. 198
Seq#:4; Xaa Pos. 198





DATE: 05/30/2002

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/689,343B TIME: 10:22:33

Input Set : A:\NEB-181.ST25.txt

Output Set: N:\CRF3\05302002\1689343B.raw

L:259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:576 L:260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:624 L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:192